

Fig. 1

Aldotetrose (4)	Dery D-Erythrose
	DThr D-Threose
	Lery L-Erythrose
	LThr L-Threose
Ketotetrose (2)	Dery D-Erythrulose
	Lery L-Erythrulose
Tetritol (3)	D,LEry D,L-Erythrulose
	DThr D-Threitol
(Tetroses 9)	LThr L-Threitol
Aldopentose (8)	DRib D-Ribose
	DARA D-Arabinose
	DXyl D-Xylose
	DLyx D-Lyxose
Ketopentose (4)	LRib L-Ribose
	LARA L-Arabinose
	LXyl L-Xylose
	LLyx L-Lyxose
Pentitol (4)	DRib D-Ribulose
	DXyl D-Xylulose
	LRib L-Ribulose
	LXyl L-Xylulose
(Pentoses 16)	D,LRib D-Ribitol,L-Ribitol
	DARA D-Arabitol
	D,LXyl D-Xylitol,L-Xylitol
	LARA L-Arabitol
Aldohexose (16)	DAlI D-Allose
	DAlt D-Altrose
	DGlu D-Glucose
	DMan D-Mannose
	DGuI D-Gulose
	DIdo D-Idose
	DGal D-Galactose
	DTal D-Talose
	LAlI L-Allose
	LAlt L-Altrose
	Lglu L-Glucose
	LMan L-Mannose
	LGuI L-Gulose
	LIdo L-Idose
	LGal L-Galactose
	LTal L-Talose
Ketohexose (8)	DFru D-Fructose
	DPsi D-Psicose
	DSor D-Sorbose
	DTag D-Tagatose
	LFru L-Fructose
	LPsi L-Psicose
	LSor L-Sorbose
	LTag L-Tagatose
Hexitol (10)	D,LAlI D-Allitol,L-Allitol
	DAlt,DTal D-Altritol,D-Talitol
	DGuI,LGuI D-Glucitol,L-Gulitol
	DMan D-Manitol
	DGuI,LGuI D-Gulitol,L-Glucitol
	DIdi D-Iditol
	D,LGal D-Galactitol,L-Galactitol
	LAlt,LTal L-Altritol,L-Talitol
	LMan L-Mannitol
	LIdi L-Iditol
(Hexoses 34)	

Biosynthesis strategy for all monosaccharides using Izumoring

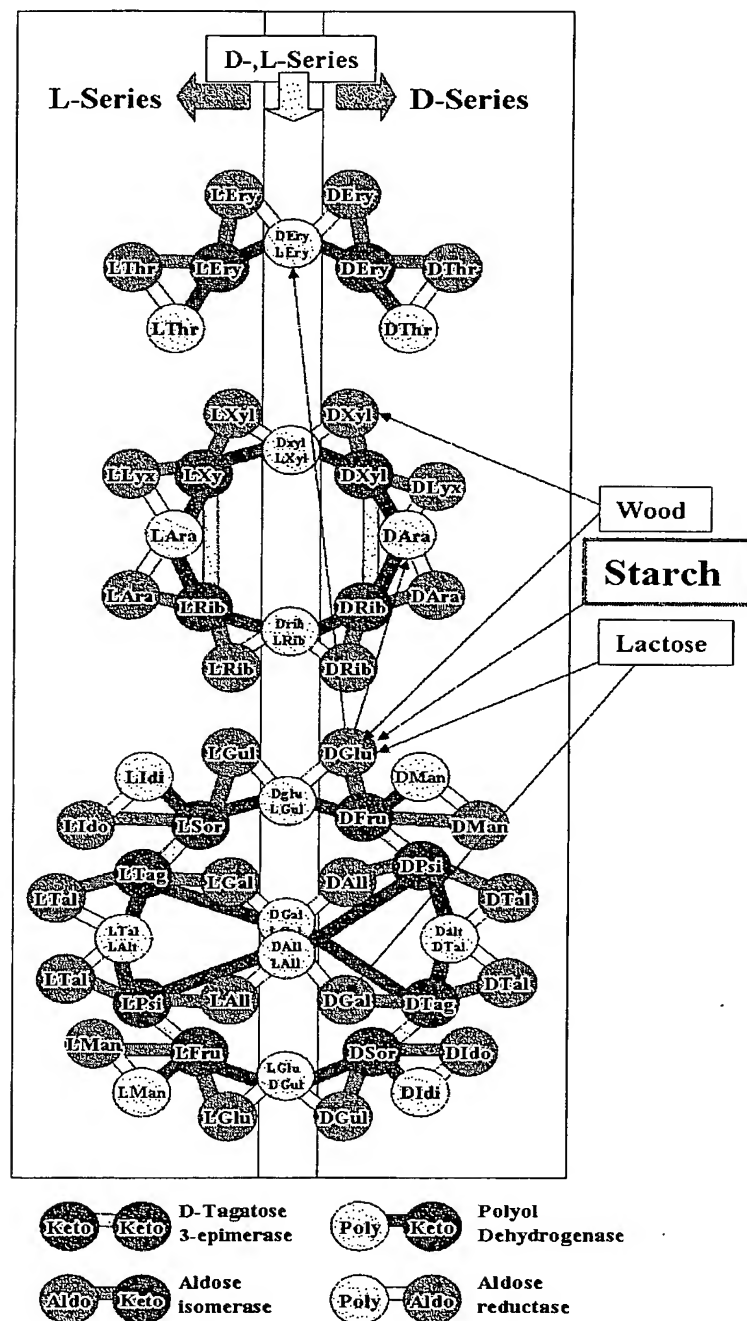


Fig. 2

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1 ATGGCTGAATTCAGGATCGCTCAGGATGTCGTTGCGCGGGAAAACGACAGGCGCGCCTCG 60
1 M A E F R I A Q D V V A R E N D R R A S 20
61 GCGCTGAAGGAAGACTACGAGGCGCTCGGCGCGAATCTCGCCGCGGTGGCGTCGACATC 120
21 A L K E D Y E A L G A N L A R R G V D I 40
121 GAGGCGGTACGCGCAAGGTCGAAAAGTTCTTCGTCGCGCTCCCCTCCTGGGGCGTCGGC 180
41 E A V T A K V E K F F V A V P S W G V G 60
181 ACGGGCGGCACGCGCTTTGCGCGCTTCCCCGGCACCGGCGAGCCGCGCGGCATCTTCGAC 240
61 T G G T R F A R F P G T G E P R G I F D 80
241 AAGCTGGACGACTGCGCGTCATCCAGCAGCTGACACGCGCCACGCCAATGTCTCGCTG 300
81 K L D D C A V I Q Q L T R A T P N V S L 100
301 CATATTCCGTGGGACAAGGCCGATCCGAAGGAGCTGAAGGCCAGGGGCGACGCCCTCGGC 360
101 H I P W D K A D P K E L K A R G D A L G 120
361 CTCGGCTTCGACGCGATGAATCCAATACCTTCTCCGATGCGCCCGGCCAGGGCGATTCC 420
121 L G F D A M N S N T F S D A P G Q A H S 140
421 TACAAATACGGCTCGCTCAGCCACACGGATGCGGCAACGCGCGCCAGGCGGTGAGCAC 480
141 Y K Y G S L S H T D A A T R A Q A V E H 160
481 AATCTGGAATGCATCGAGATCGGCAAGGCCATCGGCTCCAAGGCGCTGACGGTCTGGATC 540
161 N L E C I E I G K A I G S K A L T V W I 180
541 GGTGACGGCTCCAACCTTCCCCGGCCAGAGTAACCTCACCAGGGCTTTGAAAGTTATCTC 600
181 G D G S N F P G Q S N F T R A F E R Y L 200
601 TCGGCGATGGCGGAGATCTACAAGGGCCTGCCGATGACTGGAAGCTGTTCTCCGAGCAC 660
201 S A M A E I Y K G L P D D W K L F S E H 220
661 AAGATGTACGAGCGGCCTTCTATTGACCGTCTGTCAGGACTGGGGCACGAATTATCTC 720
221 K M Y E P A F Y S T V V Q D W G T N Y L 240
721 ATCGCCAGACGCTCGGCCCCAAGGCCAGTGCCTCGTCGATCTCGGCCATCACGCGCCG 780
241 I A Q T L G P K A Q C L V D L G H H A P 260
781 AACACCAATATCGAGATGATCGTCGCGCGCTCATCCAGTTCCGCAAGCTCGGCGGCTTC 840
261 N T N I E M I V A R L I Q F G K L G G F 280
841 CATTTCAACGATTCCAATACGGCGACGACGACCTCGATGCCGGCGCCATCGAGCCCTAT 900
281 H F N D S K Y G D D D L D A G A I E P Y 300
901 CGCCTCTTCTCGTCTTCAACGAGCTGGTGGATGCGGAGGCGCGCGCTCAAGGGCTTC 960
301 R L F L V F N E L V D A E A R G V K G F 320
961 CACCGGGCCACATGATCGACCAATCGCACACGTCACCGACCCGATCGAGAGCCTGATC 1020
321 H P A H M I D Q S H N V T D P I E S L I 340
1021 AACAGCGCGAAGCAATCCGTGCGCGCTATGCGCAGGCCCTCCTTGTGACCGCGCGGGC 1080
341 N S A N E I R R A Y A Q A L L V D R A A 360
1081 CTTTCCGGCTACCAGGAGGACAACGACGCCCTGATGGCGACGGAACGTTGAAGCGCGCC 1140
361 L S G Y Q E D N D A L M A T E T L K R A 380
1141 TACCGTACCGATGTGGAGCCGATCCTCGCGAGGCGCGCGCCGACGGGCGGCGCGGTC 1200
381 Y R T D V E P I L A E A R R R T G G A V 400
1201 GACCCCGTCGCGACCTATCGGGCCAGCGGCTACCGCGCCAGGGTCCCGCGGAGCGCCCC 1260
401 D P V A T Y R A S G Y R A R V A A E R P 420
1261 GCCTCCGTGCGGGGTGGCGGCGGCATCATCTGA 1293
421 A S V A G G G G I I * 431
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Fig. 3

M---AEFRIAQDVVARENDRRASALKEDYEALGANLARQVDIEAVTAKVEKFFVA--VP 55  
MTIKANYDSAKQAYEKWGIDVEEALRQLEQVPSIHCVQGGDIEGFEVKNKGELSGGIDVT 60

SWGVTGGTRFARFGTGEPRGIFDKLDDCAVIQQLTRATPNVSLHIPWDKADPKELKAR 115  
GNYPGKAQTPEELRRDLEKALSLIPGKHRVNLHAIYAETNREAVERDELKPQHFENWVKW 120

GDALGLGFDAMNSNTFSDAPGQAHSYKYGSLSHTDAATRAQAVEHNLEGIEIGKAIGSKA 175  
AKNLGLGLDFNPTLFSHEKAADGLT-----LSHPDPDIREFWIRHCIACRRIGEYFGKEL 175

LTVWIGDGSNFPQGSNFTR----AFERYLSAMAEIY-KGLPDDWKLFS-EHKMYEPAFYS 229  
GTPCLTNIWIPDQYKDIPSDRLTPRKRLKESLDRIFSEEISEQHNLDSIESKLFGLGSES 235

TVVQDWGTNYLIAQTLGPKAQCLVDLGH-HAPNTNIEMIVARLIQFGKLGGFHFNDISKY 288  
YVV--GSHEFYLAYALTNHKLCLLDTGHFHPTETVSNKISSMLLYTDKLA-LHVS RPVRW 292

DDDL DAGAIEPYRLFLVFNELVDAEARGVKGFHPAHMIDQSHNVTDPIESLINSANEIRR 348  
DSDHVVVLDEL R-----EIALEIVRNHALEKVAIGLDFFDASINRVAAWTIGTRNMIK 346

AYAQALLVDRAALSGYQEDNDALMATETLKRAYRTDVEPI LAEARRRTGGAVDPVATYRA 408  
ALLYALLPNGYLKQLQEEGRYTERLALMEEFKTYPFGAIVDSYCEQMGVPVKEAWLYDI 406

SGYRARVAAERPASVAGGGGII 430  
KEYEQQVLLKRKASSP----IV 424

上: *Pseudomonas stutzerii*

下: *Bacillus subtilis*

Fig. 4

RhI	MAEFR I AQDVVARENDRRASAL KEDYEAL GANLARRGVD I EAVTAKVEKFFVAVPSWVG	60
SISTR	NTE-----LA AVKAALKTQAVETPSWAYG	24
SITHE	MI-----NMER I FKELDELKFELPSWAFS	24
RhI	TGGTRFARFPGTGEPRI FDKLDDCAV I QQL TRATPNVSLHI PWDKA-DPKELKARGDAL	119
SISTR	NSGTRFKVF AQPGVPRDPF EKLDAAKVHEFT GAAPTVALHI PWRVEDYAAL AAHAER	84
SITHE	DAGTRFAVHEEGAARNVFER IEDAAL VHRL GCCPSVALHI PWDKVENWEELREFAEK	84
RhI	GLGFDAMNSNTFSDAPGQAHSYKYGSLSHTDAATRAQAVEHNLECI E I GKA I GSKALTVW	179
SISTR	GVR I GA I NSNTFQDD-----DYRLGS I CHPDAAVRRKAVDHLL ECVD I MDATGSRDLKLW	139
SITHE	GLK I GA I NPNLFQDP-----DYKYGSLTNPSEK I RKKA I AHVMECVD I AEKTGSKV I SLW	139
RhI	I GDGSNFPGQSNFTRAFERYLSAMAE I YKGLPDDWKL FSEHKMYEPAFYSTVVDWGTNY	239
SISTR	FADGTNYPGQDD I RSRQDRLAEGLAEVYERL GEGQRM LLEYKLFEPAFYTIDVPDWTAY	199
SITHE	LADGTDYPGQDDFRSRKKRLEESLRY I YENMPADMYLL I EYKFFEPAFYHTDIPDWGMSY	199
RhI	L I AQTLGPKAQCLVDLGHHPNTN I EM I VARL I QFGKLGGFHFND SKYGDDDL DAGA I EP	299
SISTR	AHCLKLGEKAQVVVD TGHHAPGTN I EF I VATLLREGKLGGFDFNSRFYADDDL MVGAADP	259
SITHE	LLSEKLGERALVLVDLGHHPQGTN I EY I VATLLSEKKLGGFHLNNRKYADDDL T I AS I NP	259
RhI	YRLFVFNELVDAEARGVKGFH-----PAHMI DQSHNVTDPI ESL I NSANE I RRAYAQALL V	356
SISTR	FQLFRI-----MYEVVRGGGFTSD-----VAFMLDQCHNI EAK I PA I RSVMNVQEATAKALL V	313
SITHE	YEVEL I FKE I VFAKRDP ELSDSAKKVVL MFDGAH I TKPK I LAM I QSVL I AQELFTKALL I	319
RhI	DRAALSGYQEDNDALMATETL KRAYRTDVEPI LAEARRRTGGAVDPVATYRASGYRARVA	416
SISTR	DGTALAEAGAAGDVLEANAVIMDAYNTDVRPLL REVREESGLDPEPMKAYRSCGWAEKV	373
SITHE	DENRLREAQKNYDVVEAE I ILDAFRTDVRPI LREYRRQKGLPEDPLRVFREEDYMEKRR	379
RhI	AERPASVAGGGG I I	430
SISTR	AER I GGQAGWG-A	386
SITHE	RERR-----	383

Fig. 5

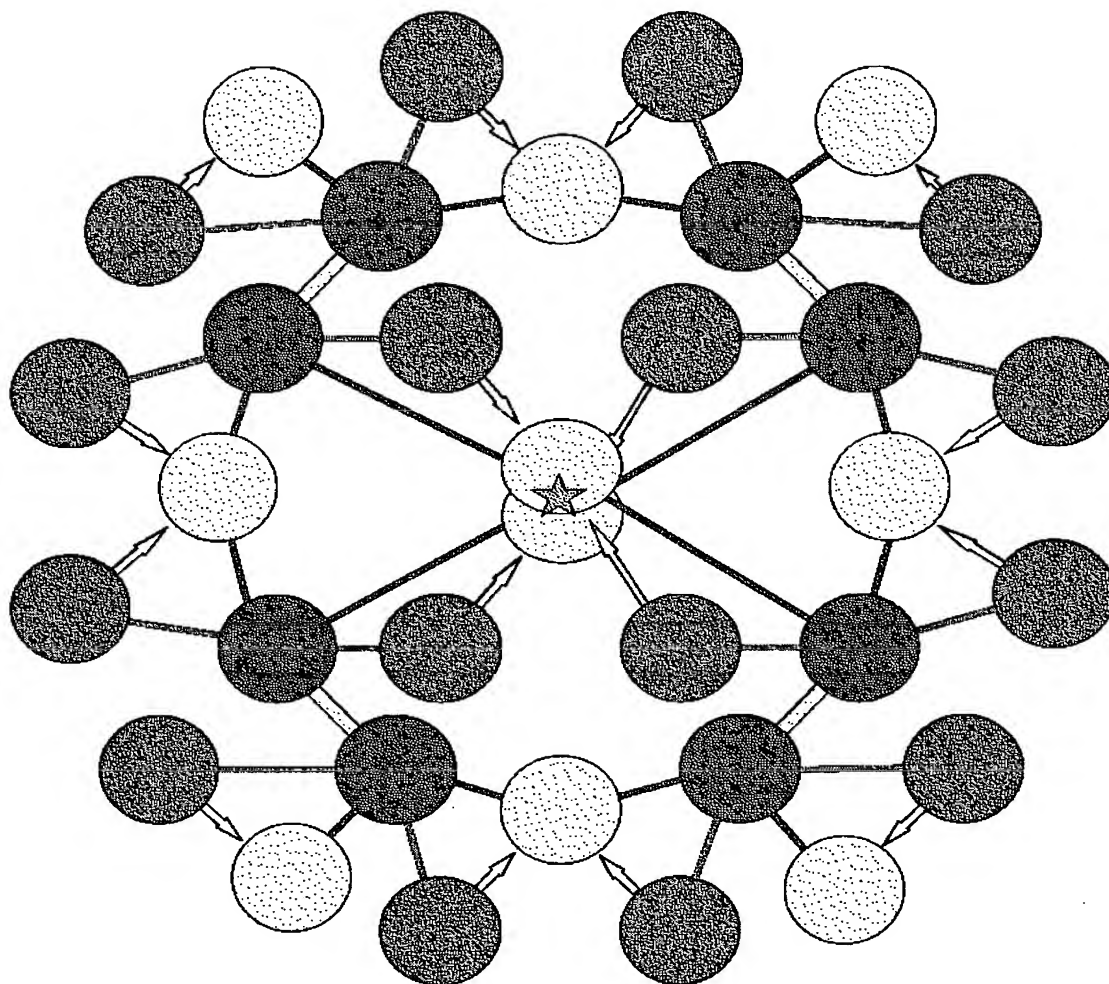


Fig. 6

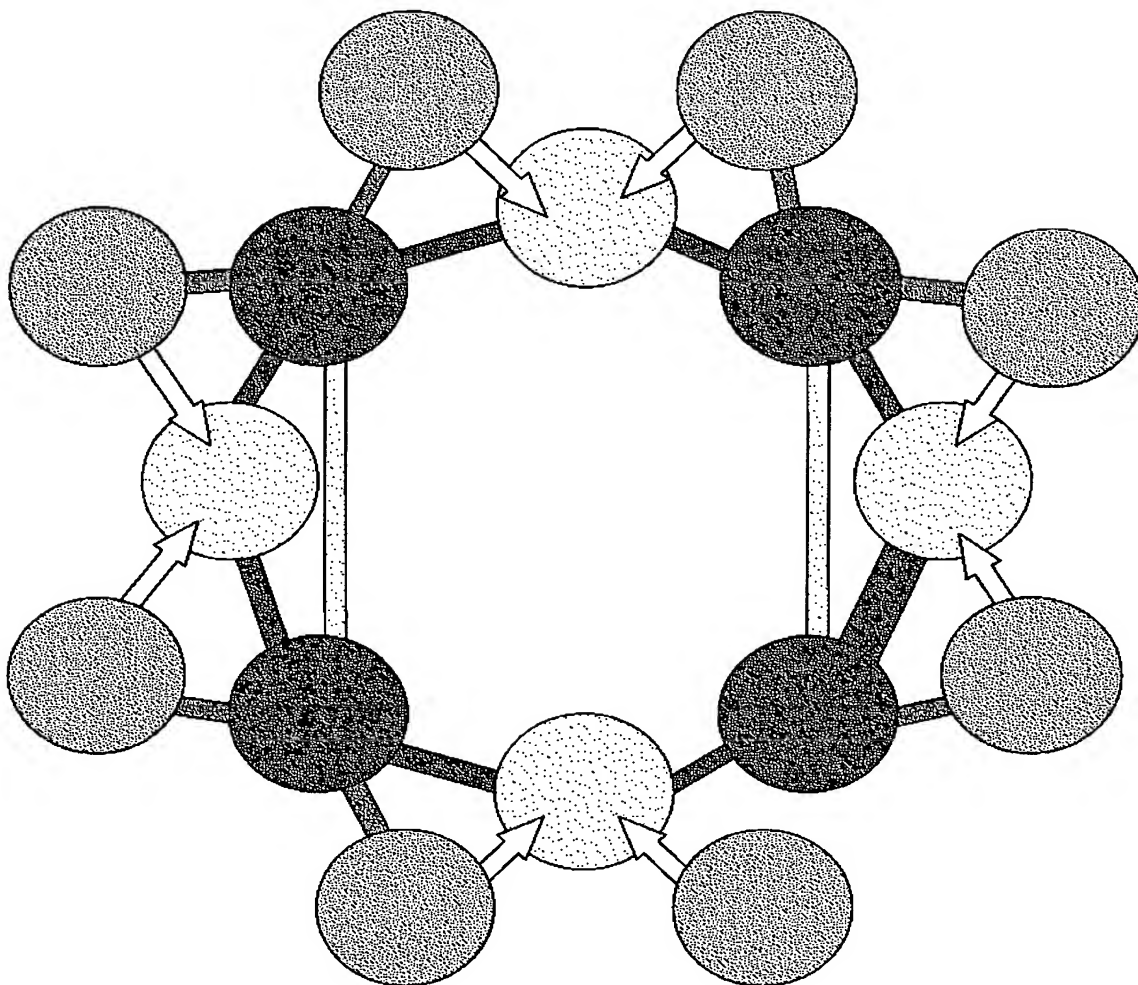


Fig. 7

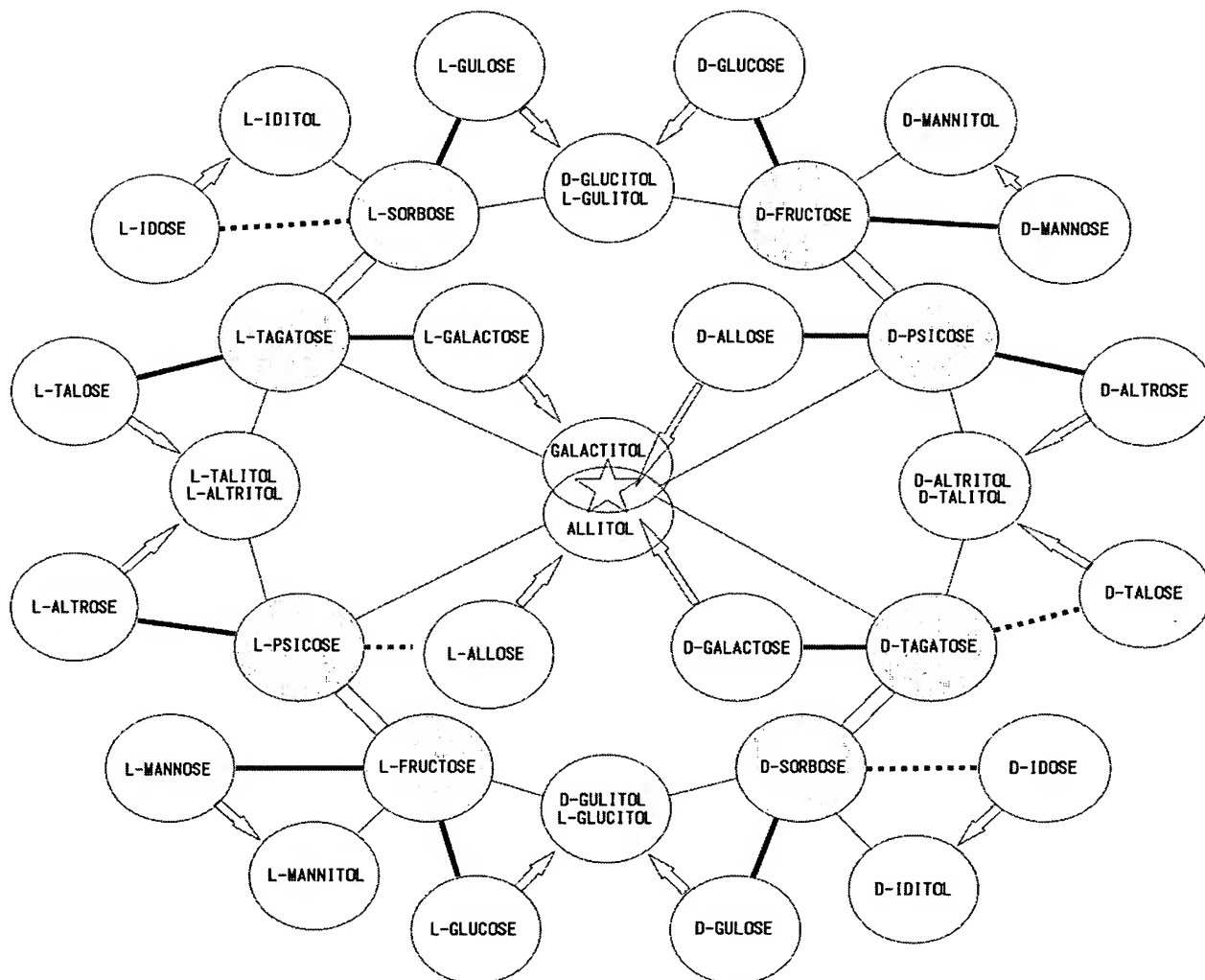


Fig. 8

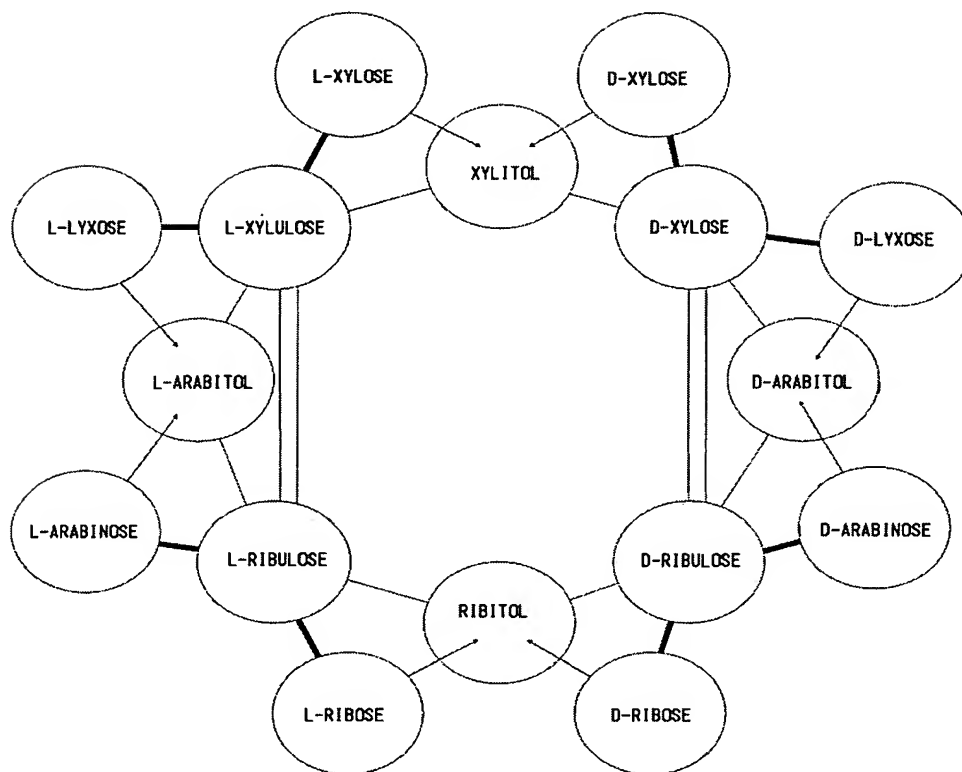




Fig. 9

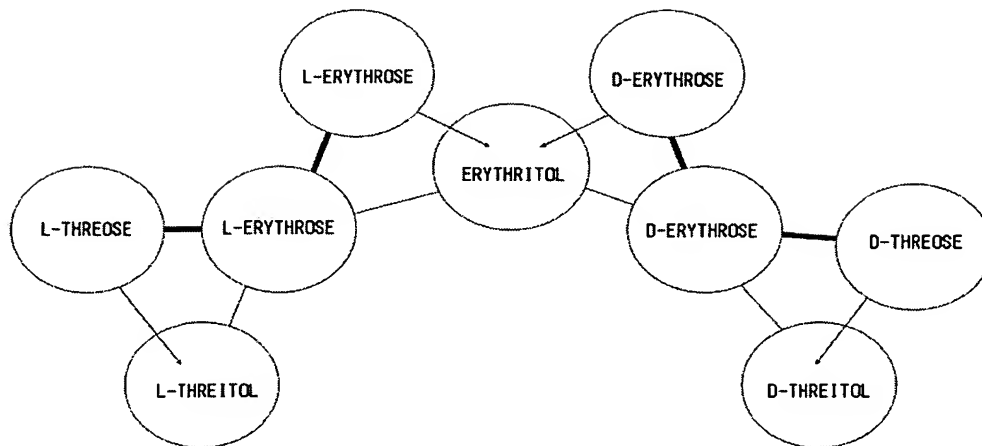


Fig. 10

